**In the Specification:**

Please amend the specification as follows:

Please delete paragraphs [0013-0017] and replace them with the following amended paragraphs:

**Figure 1:** Shows the primary structure of human EPO (165 amino acids) **(SEQ ID NO: 1)**.

**Figure 2:** Shows the primary structure of human EPO (166 amino acids) **(SEQ ID NO: 2)**.

**Figure 3:** Shows the primary structure and corresponding nucleic acid sequence **(SEQ ID NO: 6)** of the APPRIEGR-EPO **(SEQ ID NO: 3)**. The underlined amino acid sequence corresponds to the secretion signal sequence, the wavy line to the amino acid sequence specific for the proteolytic cleavage site.

**Figure 4:** Shows the primary structure and corresponding nucleic acid sequence **(SEQ ID NO: 7)** of APP-EPO **(SEQ ID NO: 4)**. The underlined amino acid sequence corresponds to the secretion signal sequence, the wavy line to the amino acid sequence specific for the proteolytic cleavage site.

**Figure 5:** Shows the primary structure and corresponding nucleic acid sequence **(SEQ ID NO: 8)** of APPGAAHY-EPO **(SEQ ID NO: 5)**. The underlined amino acid sequence corresponds to the secretion signal sequence, the wavy line to the amino acid sequence specific for the proteolytic cleavage site.

Please delete paragraph [0054] and replace it with the following amended paragraph:

Suitable proteases for cleavage of fusion proteins are described by Carter, P: Site-specific proteolysis of fusion proteins; Protein Purification: From Molecular Mechanisms to Large Scale Processes, ACS, Washington DC, pp. 181 - 193 (1990). Such proteases require a narrow specificity to cleave selectively at their recognition sequence and not anywhere in the target protein sequence. Examples are factor Xa which cleaves at IEGR↓ **(SEQ ID NO: 9)** and enterokinase which cleaves at DDDDK↓ **(SEQ ID NO: 10)**. Moreover enterokinase is reported to cleave DDDDK↓AP **(SEQ ID NO: 11)** which indicates specificity at the P1' and P2' site for interleukins (P. Carter). Enterokinase is, however, not preferred if chemical protecting agents to protect the side chain ε-amino groups of lysines have to be introduced. In such case, the enzyme would no longer work at the wanted cleaving site.

Please delete paragraph [0077] and replace it with the following amended paragraph:

A further embodiment of the invention relates to erythropoietin glycoproteins comprising the amino acid sequences as shown in Fig. 1 and Fig. 2 having a N-terminal peptidic extension which represents a proteolytic cleavage site, optionally comprising an N-terminal purification tag. Examples for these peptides are APPRIEGR-EPO **(SEQ ID NO: 3)**, APP-EPO **(SEQ ID NO: 4)** and APPGAAHY-EPO **(SEQ ID NO: 5)** (see also Figs. 3 to 5).

Please delete paragraph [0082] and replace it with the following amended paragraph:

The wild type erythropoietin coding fragment was obtained by methods known in the art, e.g. as described by Jacobs K. et al., Nature 313, 806-10 (1985). Preferably, the coding fragment

is amplified using primers EPO-EcoRI 5'-GAGCCTGAATTCACCACC **(SEQ ID NO: 12)** and EPO-SalI 5'-AGGTGGGTCGACCTGGTCAT CTGTCCCCTG **(SEQ ID NO: 13)**. The PCR fragment was digested with EcoRI and SalI (sites are underlined in primer sequences) and cloned into the multiple cloning site of the pre-digested pCI-dhfr vector fragment. Expression of the EPO gene was therefore under control of the human cytomegalovirus (CMV) immediate-early enhancer/promoter region, an optimized chimeric intron for regulated expression and the SV40 late polyadenylation signal.

Please delete paragraph [0083] and replace it with the following amended paragraph:

The APPRIEGR peptide **(residues 28-35 of SEQ ID NO: 3)** was assembled as a NarI DNA fragment by two annealed oligonucleotides APPRIEGRfor **(residues 28-35 of SEQ ID NO: 3)**, 5'-CGCCCCCCCCCGAATCGAGGGCCG **(SEQ ID NO: 14)**, and APPRIEGRrev **(residues 28-35 of SEQ ID NO: 3)**, 5'-CGCGGCCCTCGATTCGGGGGGGGG **(SEQ ID NO: 15)** (remnants of NarI site underlined), and cloned in between the N-terminal signal sequence and the mature EPO coding region.

Please delete paragraph [0085] and replace it with the following amended paragraph:

The APPGAAHY peptide **(residues 28-35 of SEQ ID NO: 5)** was assembled as a NarI DNA fragment by two annealed oligonucleotides APPGAAHYfor **(residues 28-35 of SEQ ID NO: 5)**, 5'-CGCCCCCCCCGGCGCCGCCCACTA **(SEQ ID NO: 16)**, and APPGAAHYrev **(residues 28-35 of SEQ ID NO: 5)**, 5'-CGTAGTGGGCGGCGCCGGGGGGGG **(SEQ ID NO: 17)** (remnants of NarI site underlined), and cloned in between the N-terminal signal sequence and the mature EPO coding region.